

1 GCGGCCGCGAATTCGGCACACAGGGGCGCTCTCTCCCGGTGTGGGTACTGCTGTCTGTGGT 60  
 61 GTGGCTGTGGGACCCGTGAGCAAGCAGCGACGCCAGCGGCGGAGAACCGACGAAAGGTGT 120  
 121 CACCACAGTGATGGCAGTGGAGGACAGCAGCTGCAAGTAGTGGTACGGGTGCGGCCCCC 180  
 MetAlaValGluAspSerThrLeuGlnValValValArgValArgProPr  
 181 CACCCCTCGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGT 240  
 oThrProArgGluLeuAspSerGlnArgArgProValValGlnValValAspGluArgVa  
 241 GCTGGTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCTGGCCTGAAATGGGGTGGCAC 300  
 lLeuValPheAsnProGluGluProAspGlyGlyPheProGlyLeuLysTrpGlyGlyTh  
 301 CCATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTTGG 360  
 rHisAspGlyProLysLysLysGlyLysAspLeuThrPheValPheAspArgValPheGl  
 361 CGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGACAGCTT 420  
 yGluAlaAlaThrGlnGlnAspValPheGlnHisThrThrHisSerValLeuAspSerPh  
 421 CCTCCAGGGCTACAACCTGCTCAGTGTTCCTACGGGGCCACCGGGGCTGGGAAGACACA 480  
 eLeuGlnGlyTyrAsnCysSerValPheAlaTyrGlyAlaThrGlyAlaGlyLysThrHi  
 481 CACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACCGTGGAACTGTA 520  
 sThrMetLeuGlyArgGluGlyAspProGlyIleMetTyrLeuThrThrValGluLeuTy  
 541 CAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTCATCAGCTACCAGGA 600  
 rArgArgLeuGluAlaArgGlnGlnGluLysHisPheGluValLeuIleSerTyrGlnGl

FIG. 1A

601 GGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGGCCCCTTGCCATCCGCGA 660  
 -----+-----+-----+-----+-----+-----+  
 uValTyrAsnGluGlnIleHisAspLeuLeuGluProLysGlyProLeuAlaIleArgGl  
  
 661 GGACCCCGACAAGGGGGTGGTGGTGCAAGGACTTTCTTTCCACCAGCCAGCCTCAGCCGA 720  
 -----+-----+-----+-----+-----+-----+  
 uAspProAspLysGlyValValValGlnGlyLeuSerPheHisGlnProAlaSerAlaGl  
  
 721 GCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAACCGCACGCAGCACCCCACTGATGC 780  
 -----+-----+-----+-----+-----+-----+  
 uGlnLeuLeuGluIleLeuThrArgGlyAsnArgAsnArgThrGlnHisProThrAspAl  
  
 781 CAACGCGACTTCCTCCCGCTCCCATGCCATCTTCCAGATCTTTGTGAAGCAGCAGGACCG 840  
 -----+-----+-----+-----+-----+-----+  
 aAsnAlaThrSerSerArgSerHisAlaIlePheGlnIlePheValLysGlnGlnAspAr  
  
 841 GGTTCAGGACTGACCCAGGCTGTCCAGGTGGCCAAGATGAGCCTGATTGACCTGGCTGG 900  
 -----+-----+-----+-----+-----+-----+  
 gValProGlyLeuThrGlnAlaValGlnValAlaLysMetSerLeuIleAspLeuAlaGl  
  
 901 CTCAGAGCGGGCATCCAGCACCCATGCGAAGGGGGAGCGGCTGCGGGAGGGGGCCAACAT 960  
 -----+-----+-----+-----+-----+-----+  
 ySerGluArgAlaSerSerThrHisAlaLysGlyGluArgLeuArgGluGlyAlaAsnIl  
  
 961 CAACCGCTCTCTGCTGGCGCTCATCAACGTCCTCAATGCCTTGGCCGATGCAAAGGGCCG 1020  
 -----+-----+-----+-----+-----+-----+  
 eAsnArgSerLeuLeuAlaLeuIleAsnValLeuAsnAlaLeuAlaAspAlaLysGlyAr  
  
 1021 CAAGACCCATGTGCCCTACCGGGACAGCAAAGTACCCGCTGCTCAAAGACTCCCTCGG 1080  
 -----+-----+-----+-----+-----+-----+  
 gLysThrHisValProTyrArgAspSerLysLeuThrArgLeuLeuLysAspSerLeuGl  
  
 1081 GGGCAACTGCCGCACAGTGATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGA 1120  
 -----+-----+-----+-----+-----+-----+  
 yGlyAsnCysArgThrValMetIleAlaAlaIleSerProSerSerLeuThrTyrGluAs  
  
 1141 CACGTACAACACCCTCAAATATGCCGACCGGG**GCCA**AGGAGATCAGGCTCTCGCTGAAGAG 1200  
 -----+-----+-----+-----+-----+-----+  
 pThrTyrAsnThrLeuLysTyrAlaAspArg**Ala**LysGluIleArgLeuSerLeuLysSe  
  
 1201 CAATGTGACCAGCCTGGACTGTCACATCAGCCAGTATGCTACCATCTGCCAACAGCTCCA 1260  
 -----+-----+-----+-----+-----+-----+  
 rAsnValThrSerLeuAspCysHisIleSerGlnTyrAlaThrIleCysGlnGlnLeuGl

FIG. 1B

1261 GGCTGAGGTAGCCGCTCTGAGGAAGAAGCTCCAAGTGTATGAGGGGGGAGGCCAGCCCC 1320  
 -----+-----+-----+-----+-----+-----+ 1320  
 nAlaGluValAlaAlaLeuArgLysLysLeuGlnValTyrGluGlyGlyGlyGlnProPr

1321 ACCACAGGACCTCCCAGGATCTCCCAAGTCGGGACCACCACCAGAACACCTTCCCAGCTC 1380  
 -----+-----+-----+-----+-----+-----+ 1380  
 oProGlnAspLeuProGlySerProLysSerGlyProProProGluHisLeuProSerSe

1381 CCCCTTGCCACCCACCCCTCCCAGCCAGCCCTGCACCCAGAGCTCCCTGCAGGGCCTAG 1440  
 -----+-----+-----+-----+-----+-----+ 1440  
 rProLeuProProHisProProSerGlnProCysThrProGluLeuProAlaGlyProAr

1441 AGCCCTTCAAGAGGAGAGTCTGGGGATGGAGGCCAGGTGGAGAGGGCCATGGAAGGGAA 1500  
 -----+-----+-----+-----+-----+-----+ 1500  
 gAlaLeuGlnGluGluSerLeuGlyMetGluAlaGlnValGluArgAlaMetGluGlyAs

1501 CTCTTCAGACCAGGAGCAGTCCCCAGAGGATGAGGATGAAGGCCAGCTGAGGAGGTTCC 1560  
 -----+-----+-----+-----+-----+-----+ 1560  
 nSerSerAspGlnGluGlnSerProGluAspGluAspGluGlyProAlaGluGluValPr

1561 AACCCAGATGCCAGAGCAGAACCCACACATGCACTGCCAGAGTCCCCTCGCCTGACCCT 1620  
 -----+-----+-----+-----+-----+-----+ 1620  
 oThrGlnMetProGluGlnAsnProThrHisAlaLeuProGluSerProArgLeuThrLe

1621 GCAGCCCAAGCCAGTCGTGGGCCACTTCTCAGCACGGGAAGTGGATGGGGACCGTTCTAA 1680  
 -----+-----+-----+-----+-----+-----+ 1680  
 uGlnProLysProValValGlyHisPheSerAlaArgGluLeuAspGlyAspArgSerLy

1681 GCAGTTGGCCCTAAAGGTGCTGTGCGTTGCCAGCGGCAGTACTCCCTGCTCCAAGCAGC 1740  
 -----+-----+-----+-----+-----+-----+ 1740  
 sGlnLeuAlaLeuLysValLeuCysValAlaGlnArgGlnTyrSerLeuLeuGlnAlaAl

1741 CAACCTCCTGACGCCCACATGATCACAGAGTTTGAGACCCTACAGCAGCTGGTGCAAGA 1800  
 -----+-----+-----+-----+-----+-----+ 1800  
 aAsnLeuLeuThrProAspMetIleThrGluPheGluThrLeuGlnGlnLeuValGlnGl

1801 GGAAAAAATTGAGCCTGGGGCAGAGGCCTTGAGGACTTCAGGCCTGGCCAGGGGGGCACC 1860  
 -----+-----+-----+-----+-----+-----+ 1860  
 uGluLysIleGluProGlyAlaGluAlaLeuArgThrSerGlyLeuAlaArgGlyAlaPr

1861 TCTGGCTCAGGAGCTGTGTTTCAAGTCAATCCCTGTGCCGTCTCCTCTCTGCCAGAGCC 1920  
 -----+-----+-----+-----+-----+-----+ 1920  
 oLeuAlaGlnGluLeuCysSerGluSerIleProValProSerProLeuCysProGluPr

FIG. 1C

1921 TCCAGGATACACTGGCCCTGTGACCCGGACTATGGCGAGGCGACTGAGTGGCCCCCTGCA 1980  
 oProGlyTyrThrGlyProValThrArgThrMetAlaArgArgLeuSerGlyProLeuHi  
 1981 CACCCTGGGAATCCCGCCTGGACCCAACCTGCACCCCAGCCCAGGGGTCCCGATGGCCCAT 2040  
 sThrLeuGlyIleProProGlyProAsnCysThrProAlaGlnGlySerArgTrpProMe  
 2041 GGAGAAGAAGAGGAGGAGACCAAGCGCCTTGGAGGCAGACAGTCCCATGGCCTCAAAGCG 2100  
 tGluLysLysArgArgArgProSerAlaLeuGluAlaAspSerProMetAlaSerLysAr  
 2101 GGGCACCAAGCGCCAGCGCCAGTCCTTCCTGCCCTGCCTAAGGAGAGGGTCTCTGCCTGA 2160  
 gGlyThrLysArgGlnArgGlnSerPheLeuProCysLeuArgArgGlySerLeuProAs  
 2161 CACCCAACCTTCACAGGGGCCAGCACCCCCAAAGGAGAAAGGGCCTCCTCCCCCTGCCA 2220  
 pThrGlnProSerGlnGlyProSerThrProLysGlyGluArgAlaSerSerProCysHi  
 2221 TTCCCCTCGCGTTTGGCCAGCCACAGTCATCAAAGCCGGGTGCCCTGGGCCCTTCCGC 2280  
 sSerProArgValCysProAlaThrValIleLysSerArgValProLeuGlyProSerAl  
 2281 CATGCAGAACTGCTCCACCCCGCTGGCTCTGCCCACCTCGAGACCTCAATGCCACCTTTGA 2340  
 aMetGlnAsnCysSerThrProLeuAlaLeuProThrArgAspLeuAsnAlaThrPheAs  
 2341 TCTCTCTGAGGAGCCTCCCTCAAAGCCCAGTTTCCATGAATGCATTGGCTGGGACAAAAT 2400  
 pLeuSerGluGluProProSerLysProSerPheHisGluCysIleGlyTrpAspLysIl  
 2401 ACCCCAGGAGCTGAGCAGGCTGGACCAGCCCTTCATCCCCAGGGCACCTGTGCCCTGTT 2460  
 eProGlnGluLeuSerArgLeuAspGlnProPheIleProArgAlaProValProLeuPh  
 2461 CACCATGAAGGGCCCCAAGCCAACATCTTCCCTCCCTGGGACCTCTGCCTGCAAGAAGAA 2520  
 eThrMetLysGlyProLysProThrSerSerLeuProGlyThrSerAlaCysLysLysLy  
 2521 GCGCGTTGCGAGTTCCTCAGTCTCCCATGGCCGAGCCGCATCGCCCGCTCCCCAGCAG 2580  
 sArgValAlaSerSerSerValSerHisGlyArgSerArgIleAlaArgLeuProSerSe

FIG. 1D

2581 CACTTTGAAGAGGCCAGCTGGGCCCCTTG TACTCCCAGAGCTGCCCTTGAGTCCCCTGTG 2640  
 -----+-----+-----+-----+-----+-----+-----+  
 rThrLeuLysArgProAlaGlyProLeuValLeuProGluLeuProLeuSerProLeuCy  
  
 2641 CCCTAGCAACCGGAGGAATGGAAAGGACCTCATCAGGGTGGGGAGAGCGCTCTCAGCAGG 2700  
 -----+-----+-----+-----+-----+-----+-----+  
 sProSerAsnArgArgAsnGlyLysAspLeuIleArgValGlyArgAlaLeuSerAlaGl  
  
 2701 GAACGGCGTCACCAAGGTGTCCTGACCGCCAGAATGTCCTGACCACCAAGGTGTCCTAAC 2760  
 -----+-----+-----+-----+-----+-----+-----+  
 yAsnGlyValThrLysValSer  
  
 2761 CTACCGGCCCCTCTGCTGGATACCCCTCTTGGACCTGTAGCCACCTGCACCAGGAGCTGG 2820  
 -----+-----+-----+-----+-----+-----+-----+  
  
 2821 ACCTGCCTTCCTTACCTGGGAGCAATTAGTGCCAACACACCTTTGCTGTATTAACATCCC 2880  
 -----+-----+-----+-----+-----+-----+-----+  
  
 2881 TCCCCAGACATCCATCCTGCTACTCACCTCTGTTAATCTCCTGTTACACTCAGCTTCTT 2940  
 -----+-----+-----+-----+-----+-----+-----+  
  
 2941 GGCATGTACATATTCATTTGTGAGTGTTAATGTGCTGCTGTTTTTTGTTTTTTGGTGTT 3000  
 -----+-----+-----+-----+-----+-----+-----+  
  
 3001 TTTGTTTTTTGTTTTTTTTGTTTTGAGATGGAGTCTTACTCTGTCGCCCAGGCTGGAGTG 3060  
 -----+-----+-----+-----+-----+-----+-----+  
  
 3061 CAGTGGTACGATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGTAATTCTCCTGC 3120  
 -----+-----+-----+-----+-----+-----+-----+  
  
 3121 CTCAGCTTTCCAAGTAGCTGGGATTACAGGCACCCATCACCACACCCAGCTAATTTTCGT 3180  
 -----+-----+-----+-----+-----+-----+-----+  
  
 3181 CTTTTTAATAGAGAGGGGGTTTTTCCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTC 3240  
 -----+-----+-----+-----+-----+-----+-----+  
  
 3241 AGGTGATCCGCCTGCCTCAGCTTCCCAAAGTGCTGAGATTACAGGCATGAGCTACCACGC 3300  
 -----+-----+-----+-----+-----+-----+-----+  
  
 3301 CTGGCCCGTGTTGCTGTTTTTAAAGGTGCTGCCATGTTCCCCCATCTTTTTTTTTTTGAG 3360  
 -----+-----+-----+-----+-----+-----+-----+

FIG. 1E

3361 ATGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGTGGCGATCTTGGCTCACTGCA 3420  
 -----+-----+-----+-----+-----+-----+-----+  
 3421 AGCTCCGCCTCCCAGGTTACACCATTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA 3480  
 -----+-----+-----+-----+-----+-----+-----+  
 3481 CAGGCGCCCAACCACGCGCCGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCAC 3540  
 -----+-----+-----+-----+-----+-----+-----+  
 3541 CGTGTTAGCCAGGCTGGTCTCGATCTGACCTCATGATCCACCCGCCTCGGCCTCCCAAAG 3600  
 -----+-----+-----+-----+-----+-----+-----+  
 3601 TGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCTCCCCTCTCATTTATGATGCCCTC 3660  
 -----+-----+-----+-----+-----+-----+-----+  
 3661 TGTGCAGGCAGACGGCTCTTGGGCTCTTTCCCCACCTGTCTCTAACACAGGCCCCACGG 3720  
 -----+-----+-----+-----+-----+-----+-----+  
 3721 TGATGGCCACAGGCAGTAGAGGAGGAATGAGGATGGGTGCGGGAGCGGGGAGTCGCGGCT 3780  
 -----+-----+-----+-----+-----+-----+-----+  
 3781 TGGCTCTTCCTGGTTTCTGAGAGGGACATCTTCATCCCTACTCCCCTTGGTCCCCAACCA 3840  
 -----+-----+-----+-----+-----+-----+-----+  
 3841 CAGTCCTGGTGAAGATGTGGATGATAATGGTGCCTTGATTTCCAAATGAAGACAGCTTTA 3900  
 -----+-----+-----+-----+-----+-----+-----+  
 3901 TTGCTTAACTCTATTGTACATAGGATACACGTTTCAGTGTAAAATAAAGTGTAAGGGGAA 3960  
 -----+-----+-----+-----+-----+-----+-----+  
 3961 TTCAGGCTTAATGCTGCACCTAGATATAAATGCTAATGATACTTGGGTTTATAGCCTTCT 4020  
 -----+-----+-----+-----+-----+-----+-----+  
 4021 GATCCTTTATTTCTGCATATATATAGATATATACATATATTTTGGGTATAACAATAAA 4080  
 -----+-----+-----+-----+-----+-----+-----+  
 4081 CCGTCTCCATCCTTGGGAAAAAAAAAAAA 4108  
 -----+-----+-----+-----+-----+-----+-----+

FIG. 1F



1 GACAGCACGC TGCAAGTAGT GGTACGGGTG CGGCCCCCA CCCCTCGGGA GCTGGACAGT  
61 CAGCGGCGGC CAGTGGTTCA GGTGGTGGAC GAGCGGGTGC TGGTGTTTAA CCCTGAGGAG  
121 CCCGATGGAG GGTTCCTTGG CCTGAAATGG GGTGGCACCC ATGATGGCCC CAAGAAGAAG  
181 GGCAAAGACC TGACGTTTGT CTTTGACCGG GTCTTTGGCG AGGCGGCCAC CCAACAGGAC  
241 GTGTTCCAGC ACACCACGCA CAGCGTCCTG GACAGCTTCC TCCAGGGCTA CAACTGCTCA  
301 GTGTTTGCCT ACGGGGCCAC CGGGGCTGGG AAGACACACA CCATGCTGGG AAGGGAGGGG  
361 GACCCCGGCA TCATGTACCT GACCACCGTG GAACTGTACA GGCGCCTGGA GGCCCGCCAG  
421 CAGGAGAAGC ACTTCGAGGT GCTCATCAGC TACCAGGAGG TGTATAATGA ACAGATCCAT  
481 GACCTCCTGG AGCCCAAGGG GCCCCTTGCC ATCCGCGAGG ACCCGACAA GGGGGTGGTG  
541 GTGCAAGGAC TTTCTTTCCA CCAGCCAGCC TCAGCCGAGC AGCTGCTGGA GATACTGACC  
601 AGGGGGAACC GTAACCGCAC GCAGCACCCC ACTGATGCCA ACGCGACTTC CTCCCGCTCC  
661 CATGCCATCT TCCAGATCTT TGTGAAGCAG CAGGACCGGG TTCCAGGACT GACCCAGGCT  
721 GTCCAGGTGG CCAAGATGAG CCTGATTGAC CTGGCTGGCT CAGAGCGGGC ATCCAGCACC  
781 CATGCGAAGG GGGAGCGGCT GCGGGAGGGG GCCAACATCA ACCGCTCTCT GCTGGCGCTC  
841 ATCAACGTCC TCAATGCCTT GGCCGATGCA AAGGGCCGCA AGACCCATGT GCCCTACCGG  
901 GACAGCAAAC TGACCCGCCT GCTCAAAGAC TCCCTCGGGG GCAACTGCCG CACAGTGATG  
961 ATCGCTGCCA TCAGCCCCTC CAGCCTGACC TACGAGGACA CGTACAACAC CCTC

FIG. 2

1 DSTLQVVVRV RPPTPRELDS QRRPVVQVVD ERVLVFNPEE PDGGFPGLKW GGTHDGPKKK  
61 GKDLTFVFDR VFGEAATQOD VFQHTTHSVL DSFLQGYNCS VFAYGATGAG KTHTMLGREG  
121 DPGIMYLTTV ELYRRLEARQ QEKHFEVLIS YQEVYNEQIH DLLEPKGPLA IREDPDKGVV  
181 VQGLSFHQPA SAEQLLEILT RGNRNRTQHP TDANATSSRS HAIFQIFVKQ QDRVPGLTQA  
241 VQVAKMSLID LAGSERASST HAKGERLREG ANINRSLAL INVLNALADA KGRKTHVPYR  
301 DSKLTRLLKD SLGGNCRTVM IAAISPSSLT YEDTYNTL

FIG. 3



MAVEDSTLQVVVRVPPTPRELDSQRRPVVQVVDERVLVFNPEEPDGGFPGLKWGGT  
HDGPKKKGKDLTFVFDRVFGAATQQDVFQHTTHSVLDSFLQGYNCSVFAYGATGAG  
KTHTMLGREGDPGIMYLTTVELYRRLEARQQEKHFEVLISYQEVYNEQIHDLLLEPKG  
PLAIREDPDKGVVVQGLSFHQPASAEQLLEILTRGNRNRTQHPTDANATSSRSHAI F  
QIFVKQQDRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSLALI  
NVLNALADAKGRKTHVPYRDSKLTRLKKDSLGGNCRTVMIAAISPSSTLYEDTYNTL  
KYADRAKEIRLKGNSKLEGKPIPNPLLGLDSTRTGHHHHHH

FIG. 4

**ATGG**CAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCCACCCT  
CGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGTGCTG  
GTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCTTGGCCTGAAATGGGGTGGCACC  
CATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTT  
GGCGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGAC  
AGCTTCCTCCAGGGCTACAACCTGCTCAGTGTTCCTACGGGGCCACCGGGGCTGGG  
AAGACACACACCATGCTGGGAAGGGAGGGGACCCCGGCATCATGTACCTGACCACC  
GTGGAACGTGTACAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTC  
ATCAGCTACCAGGAGGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGG  
CCCCTTGCCATCCGCGAGGACCCCGACAAGGGGGTGGTGGTGCAAGGACTTTCTTTC  
CACCAGCCAGCCTCAGCCGAGCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAAC  
CGCACGCAGCACCCCACTGATGCCAACGCGACTTCCTCCCGCTCCCATGCCATCTTC  
CAGATCTTTGTGAAGCAGCAGGACCGGGTTCAGGACTGACCCAGGCTGTCCAGGTG  
GCCAAGATGAGCCTGATTGACCTGGCTGGCTCAGAGCGGGCATCCAGCACCCATGCG  
AAGGGGGAGCGGCTGCGGGAGGGGGCCAACATCAACCGCTCTCTGCTGGCGCTCATC  
AACGTCCTCAATGCCTTGGCCGATGCAAAGGGCCGCAAGACCCATGTGCCCTACCGG  
GACAGCAAACCTGACCCGCCTGCTCAAAGACTCCCTCGGGGGCAACTGCCGCACAGTG  
ATGATCGCTGCCATCAGCCCCCTCCAGCCTGACCTACGAGGACACGTACAACACCCTC  
AAATATGCCGACCGGGCCAAGGAGATCAGGCTCAAGGGCAATTCGAAGCTTGAAGGT  
AAGCCTATCCCTAACCCTCTCCTCGGTCTCGATTCTACGCGTACCGGTCATCATCAC  
CATCACCATTGA

FIG. 5



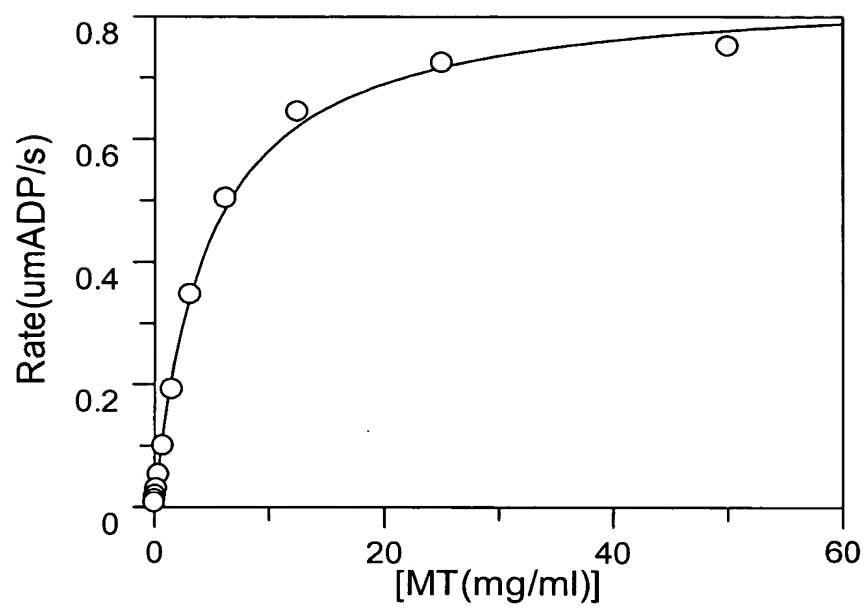


FIG. 6

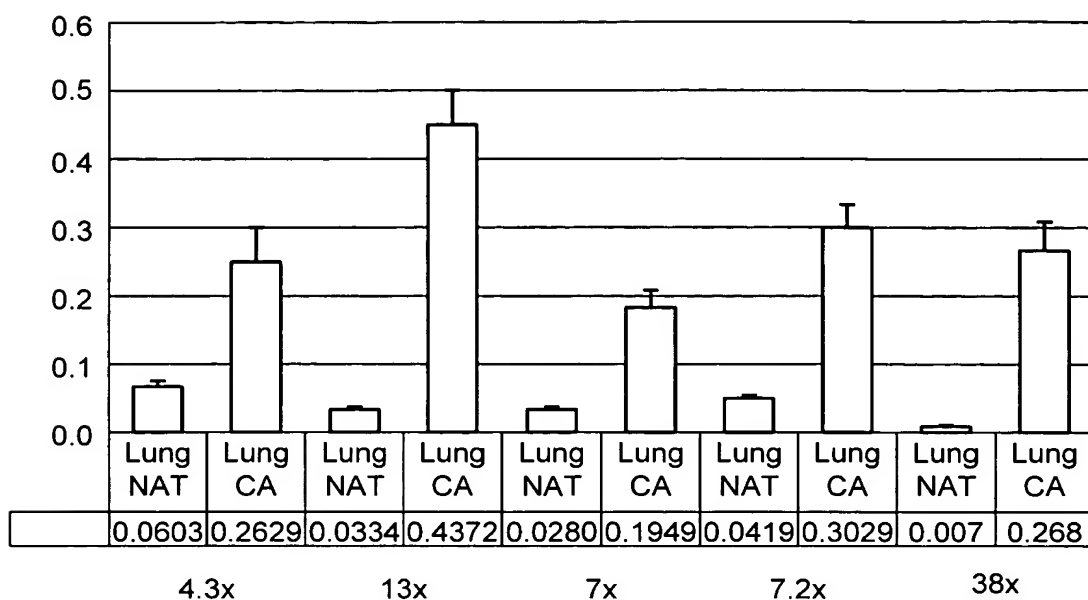


FIG. 7A

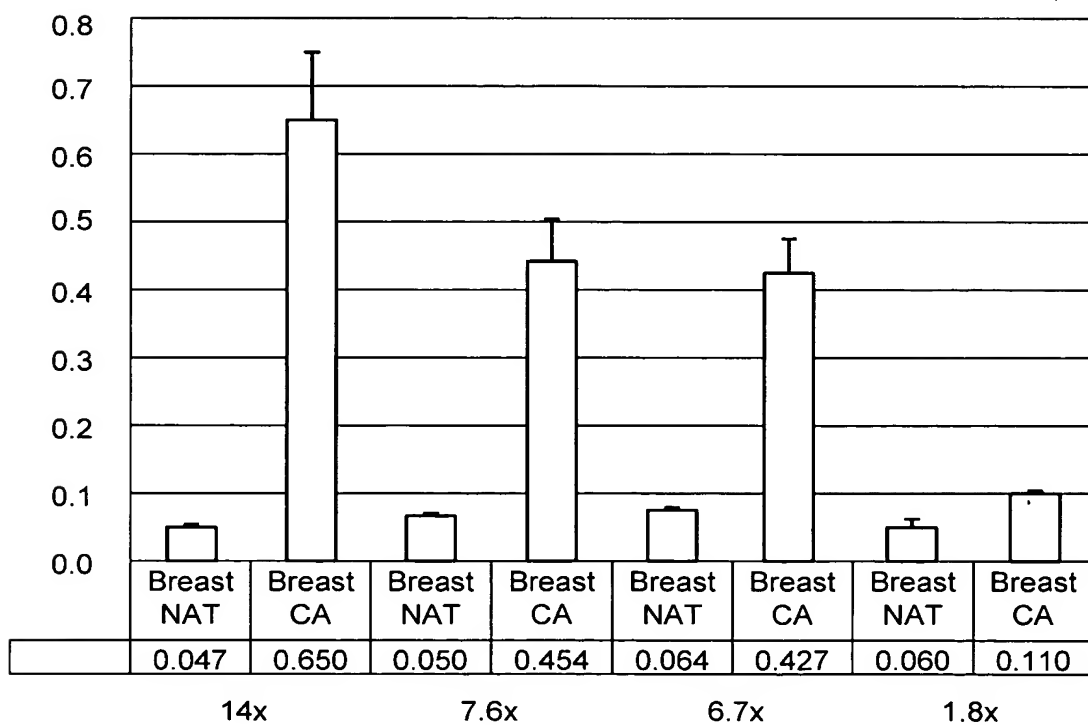


FIG. 7B

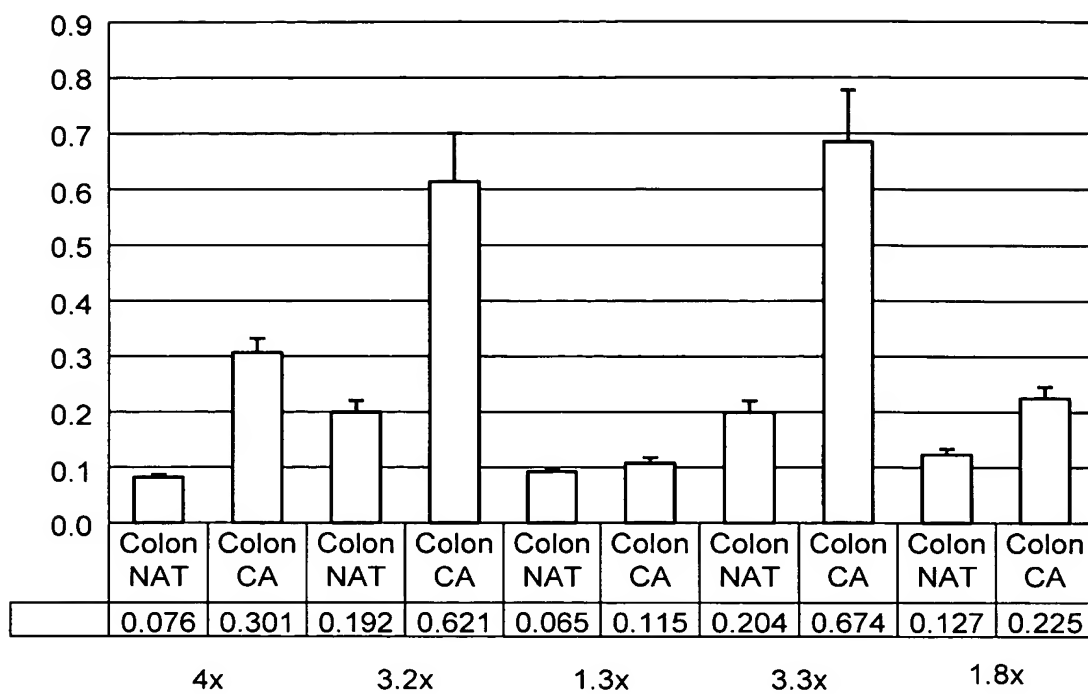


FIG. 7C

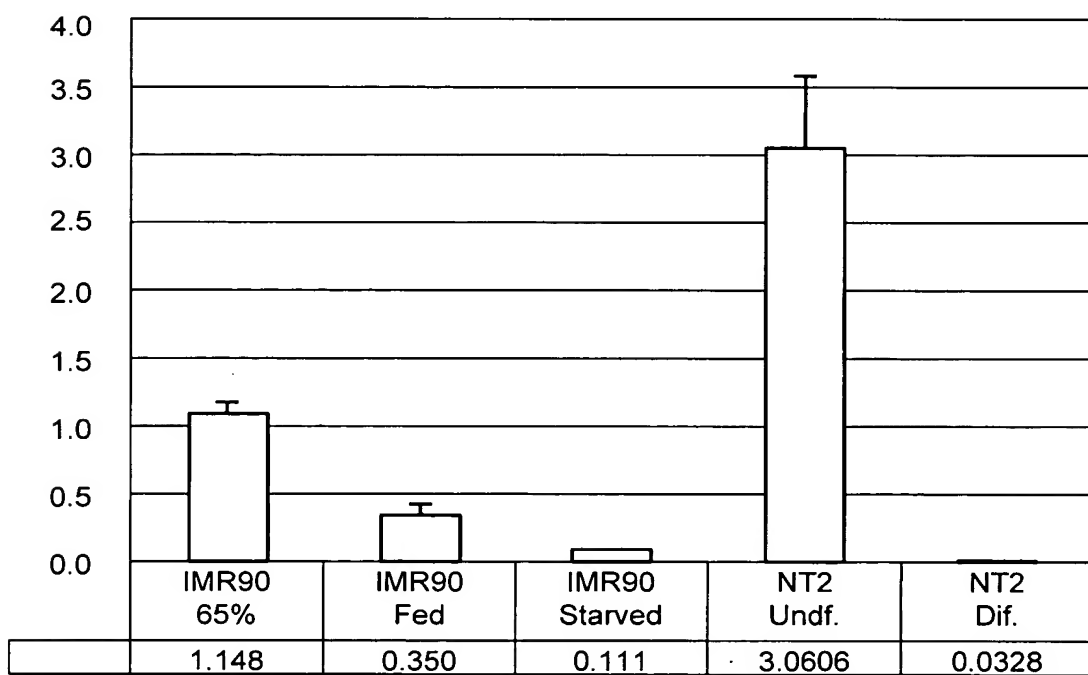


FIG. 7D